

142

SEQUENCE LISTING

T0430

(1) GENERAL INFORMATION

(i) APPLICANT: Sheppard, Paul O.

(ii) TITLE OF THE INVENTION: SERINE PROTEASE POLYPEPTIDES AND MATERIALS AND METHODS FOR MAKING THEM

(iii) NUMBER OF SEQUENCES: 18

(iv) CORRESPONDENCE ADDRESS:

(A) ADDRESSEE: ZymoGenetics, Inc.
(B) STREET: 1201 Eastlake Avenue East
(C) CITY: Seattle
(D) STATE: WA
(E) COUNTRY: USA
(F) ZIP: 98102

(v) COMPUTER READABLE FORM:

(A) MEDIUM TYPE: Diskette
(B) COMPUTER: IBM Compatible
(C) OPERATING SYSTEM: DOS
(D) SOFTWARE: FastSEQ for Windows Version 2.0

(vi) CURRENT APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:
(C) CLASSIFICATION:

(vii) PRIOR APPLICATION DATA:

(A) APPLICATION NUMBER:
(B) FILING DATE:

(viii) ATTORNEY/AGENT INFORMATION:

(A) NAME: Parker, Gary E
(B) REGISTRATION NUMBER: 31,648
(C) REFERENCE/DOCKET NUMBER: 97-16C1

(ix) TELECOMMUNICATION INFORMATION:

(A) TELEPHONE: 206-442-6673
(B) TELEFAX: 206-442-6678
(C) TELEX:

43

243

(2) INFORMATION FOR SEQ ID NO:1:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1634 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence

- (B) LOCATION: 105...1280

- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence

- (B) LOCATION: 105...161

- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

GGCACGAGGG GGAGCCGCGC GCTCTCTCCC GGCGCCCACA CCTGTCTGAG CGGCGCAGCG 60
AGCCCGGGCC CGGGCGGGCT GCTCGGCGCG GAACAGTGCT CGGC ATG GCA GGG ATT 116
Met Ala Gly Ile

CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT GGG CAA 164
Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln
-15 -10 -5 1

GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC 212
Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg
5 10 15

CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC 260
Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp
20 25 30

TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG 308
Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly Pro Gln
35 40 45

244

244

TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC AAA GAA GCC AAG CAA TAT	356
Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Lys Glu Ala Lys Gln Tyr	
50 55 60 65	
CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG ACN CAG	404
Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu Xaa Gln	
70 75 80	
GTG GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAN CNC CGA	452
Val Gly Ile Tyr Ile Leu Ser Ser Gly Asp Gly Ala Xaa Xaa Arg	
85 90 95	
GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT TAT GGC	500
Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile Tyr Gly	
100 105 110	
TAT GAC AGC AGG TTC AGC ATT TTT GGG AAG GAC TTC CTG CTC AAC TAC	548
Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr	
115 120 125	
CCT TTC TCA ACA TCA GTG AAG TTA TCC ACG GGC TGC ACC GGC ACC CTG	596
Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu	
130 135 140 145	
GTG GCA GAA AAN CAT GTC CTC ACA GCT GCC CAC TGC ATA CAC GAT GGA	644
Val Ala Glu Xaa His Val Leu Thr Ala Ala His Cys Ile His Asp Gly	
150 155 160	
AAA ACC TAT GTG AAA GGA ACC CAG AAG CTT CGA GTC GGC TTC CTA AAG	692
Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe Leu Lys	
165 170 175	
CCC AAG TTT AAA GAT GGT GGT CGA GGG GCC AAC GAC TCC ACT TCA GCC	740
Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr Ser Ala	
180 185 190	
ATG CCC GAG CAG ATG AAA TTT CAG TGG ATC CGG GTG AAA CGC ACC CAT	788
Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys Arg Thr His	
195 200 205	
GTG CCC AAG GGT TGG ATC AAG GGC AAT GCC AAT GAC ATC GGC ATG GAT	836
Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile Gly Met Asp	
210 215 220 225	

245

45

TAT GAT TAT GCC CTC CTG GAA CTC AAA AAG CCC CAC AAG AGA AAA TTT 884
Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys Arg Lys Phe
230 235 240

ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG GGC AGA 932
Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg
245 250 255

ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG GTG TAT 980
Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr
260 265 270

CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG TTG TAC CAG CAA 1028
Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln
275 280 285

TGC GAT GCC CAG CCA GGG GCC AGC GGG TAT GGG GTA TAT GTG AGG ATG 1076
Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val Tyr Val Arg Met
290 295 300 305

TGG AAG AGA CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT 1124
Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe
310 315 320

TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC 1172
Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn
325 330 335

GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG 1220
Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp
340 345 350

ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CTT 1268
Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Leu
355 360 365

CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTTAGGAGAG GCCAAATTGT TTTTT 1325
Pro Gly Ser Asn
370

GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT 1385
TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTTACT ATTTGAAAAC TGGTTTGTGT 1445
ATCATATCAT ATATCATTGA AGCAGTTGA AGGCATACTT TTGCATAGAA ATAAAAAAA 1505
TACTGATTTG GGGCAATGAG GAATATTGA CAATTAAGTT AATCTTCACG TTTTGCAAA 1565
CTTTGATTTT TATTCATCT GAACTTGTG CAAAGATTAA TATTAATAT TTGGCATACA 1625

46

AGAGATATG

1634

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Signal Sequence

(B) LOCATION: 1...19

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

Met	Ala	Gly	Ile	Pro	Gly	Leu	Leu	Phe	Leu	Leu	Phe	Leu	Leu	Cys	
														-5	
														-10	
														-15	
Ala	Val	Gly	Gln	Val	Ser	Pro	Tyr	Ser	Ala	Pro	Trp	Lys	Pro	Thr	Trp
															10
															1
Pro	Ala	Tyr	Arg	Leu	Pro	Val	Val	Leu	Pro	Gln	Ser	Thr	Leu	Asn	Leu
															15
															20
															25
Ala	Lys	Pro	Asp	Phe	Gly	Ala	Glu	Ala	Lys	Leu	Glu	Val	Ser	Ser	Ser
															30
															35
															40
Cys	Gly	Pro	Gln	Cys	His	Lys	Gly	Thr	Pro	Leu	Pro	Thr	Tyr	Lys	Glu
															50
															55
															60
Ala	Lys	Gln	Tyr	Leu	Ser	Tyr	Glu	Thr	Leu	Tyr	Ala	Asn	Gly	Ser	Arg
															65
															70
Thr	Glu	Xaa	Gln	Val	Gly	Ile	Tyr	Ile	Leu	Ser	Ser	Ser	Gly	Asp	Gly
															80
															85
															90
Ala	Xaa	Xaa	Arg	Asp	Ser	Gly	Ser	Ser	Gly	Lys	Ser	Arg	Arg	Lys	Arg
															95
															100
															105
Gln	Ile	Tyr	Gly	Tyr	Asp	Ser	Arg	Phe	Ser	Ile	Phe	Gly	Lys	Asp	Phe
															110
															115
															120
Leu	Leu	Asn	Tyr	Pro	Phe	Ser	Thr	Ser	Val	Lys	Leu	Ser	Thr	Gly	Cys
															130
															135
Thr	Gly	Thr	Leu	Val	Ala	Glu	Xaa	His	Val	Leu	Thr	Ala	Ala	His	Cys
															145
															150
Ile	His	Asp	Gly	Lys	Thr	Tyr	Val	Lys	Gly	Thr	Gln	Lys	Leu	Arg	Val
															160
															165
															170

847

Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
175 180 185
Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
190 195 200 205
Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
210 215 220
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
225 230 235
Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
240 245 250
Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
255 260 265
Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
270 275 280 285
Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Tyr Gly Val
290 295 300
Tyr Val Arg Met Trp Lys Arg Gln Gln Gln Lys Trp Glu Arg Lys Ile
305 310 315
Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
320 325 330
Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
335 340 345
Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp
350 355 360 365
Thr Val Phe Leu Pro Gly Ser Asn
370

(2) INFORMATION FOR SEQ ID NO:3:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

TGYACNGGNW SNHTNRT

17

(2) INFORMATION FOR SEQ ID NO:4:

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 17 base pairs
(B) TYPE: nucleic acid

48

748

- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

AYNADNSWNC CNGTRCA

17

(2) INFORMATION FOR SEQ ID NO:5:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

ACNGCNGSNC AYTGYAT

17

(2) INFORMATION FOR SEQ ID NO:6:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

ATRCARTGNS CNGCNGT

17

(2) INFORMATION FOR SEQ ID NO:7:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

49

WYRTNCCNWV NGGNTGG

17

8/49

(2) INFORMATION FOR SEQ ID NO:8:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

CCANCCNBWN GGNAYRW

17

(2) INFORMATION FOR SEQ ID NO:9:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

AYNRAYTAYG AYTAYGS

17

(2) INFORMATION FOR SEQ ID NO:10:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 17 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

SCRTARTCRT ARTYNRT

17

(2) INFORMATION FOR SEQ ID NO:11:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 40 base pairs

50

- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other
- (vii) IMMEDIATE SOURCE:
- (B) CLONE: ZC11667

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TATGCAGGCC AAGTGGTTT CCAGGGGGCA CTGTAAGGGC

40

- (2) INFORMATION FOR SEQ ID NO:12:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other
- (vii) IMMEDIATE SOURCE:
- (B) CLONE: ZC13508

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TCTGCTCTGT GCTGTTGG

18

- (2) INFORMATION FOR SEQ ID NO:13:

- (i) SEQUENCE CHARACTERISTICS:
- (A) LENGTH: 18 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

- (ii) MOLECULE TYPE: Other
- (vii) IMMEDIATE SOURCE:
- (B) CLONE: ZC13509

- (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

AGTCTGGCTT GGCTAAAT

18

- (2) INFORMATION FOR SEQ ID NO:14:

2051

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1656 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(ix) FEATURE:

(A) NAME/KEY: Coding Sequence

(B) LOCATION: 105...1280

(D) OTHER INFORMATION:

(A) NAME/KEY: Signal Sequence

(B) LOCATION: 105...161

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GGCACGAGGG GGAGCCGCGC GCTCTCTCCC GGCGCCCACA CCTGTCTGAG CGGCGCAGCG	60
AGCCGCGGCC CGGGCGGGCT GCTCGGCGCG GAACAGTGCT CGGC ATG GCA GGG ATT	116
Met Ala Gly Ile	

CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT GGG CAA	164
Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val Gly Gln	
-15 -10 -5 1	

GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA TAC CGC	212
Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala Tyr Arg	
5 10 15	

CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG CCA GAC	260
Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys Pro Asp	
20 25 30	

TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA CCC CAG	308
Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly Pro Gln	
35 40 45	

TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC GAA GAG GCC AAG CAA TAT	356
Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu Ala Lys Gln Tyr	
50 55 60 65	

SA

2152

CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG ACG CAG 404
Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu Thr Glu
70 75 80

GTC GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAA CAC CGA 452
Val Gly Ile Tyr Ile Leu Ser Ser Gly Asp Gly Ala Glu His Arg
85 90 95

GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT TAT GGC 500
Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Glu Ile Tyr Gly
100 105 110

TAT GAC AGC AGG TTC AGC ATT TTT GGG AAG GAC TTC CTG CTC AAC TAC 548
Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu Asn Tyr
115 120 125

CCT TTC TCA ACA TCA GTG AAG TTA TCC ACG GGC TGC ACC GGC ACC CTG 596
Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly Thr Leu
130 135 140 145

GTC GCA GAG AAG CAT GTC CTC ACA GCT GCC CAC TGC ATA CAC GAT GGA 644
Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His Asp Gly
150 155 160

AAA ACC TAT GTG AAA GGA ACC CAG AAG CTT CGA GTG GGC TTC CTA AAG 692
Lys Thr Tyr Val Lys Gly Thr Glu Lys Leu Arg Val Glu Phe Leu Lys
165 170 175

CCC AAG TTT AAA GAT GGT GGT CGA GGG GCC AAC GAC TCC ACT TCA GCC 740
Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr Ser Ala
180 185 190

ATG CCC GAG CAG ATG AAA TTT CAG TGG ATC CGG GTG AAA CGC ACC CAT 788
Met Pro Glu Glu Met Lys Phe Glu Trp Ile Arg Val Lys Arg Thr His
195 200 205

GTC CCC AAG GGT TGG ATC AAG GGC AAT GCC AAT GAC ATC GGC ATG GAT 836
Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile Glu Met Asp
210 215 220 225

TAT GAT TAT GCC CTC CTG GAA CTC AAA AAG CCC CAC AAG AGA AAA TTT 884
Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys Arg Lys Phe
230 235 240

53

12 \$3

ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG GGC AGA	932		
Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly Gly Arg			
245	250	255	
ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG GTG TAT	980		
Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu Val Tyr			
260	265	270	
CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG CTC TAC CAG CAA	1028		
Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr Gln Gln			
275	280	285	
TGC GAT GCC CAG CCA GGG GCC AGC GGG TCT GGG GTC TAT GTG AGG ATG	1076		
Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val Tyr Val Arg Met			
290	295	300	305
TGG AAG AGA CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC ATT TTT	1124		
Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly Ile Phe			
310	315	320	
TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT TTC AAC	1172		
Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp Phe Asn			
325	330	335	
GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC TAT TGG	1220		
Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys Tyr Trp			
340	345	350	
ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGT GAC ACA GTG TTC CCT	1268		
Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp Thr Val Phe Pro			
355	360	365	
CCT GGC AGC AAT TAAGGTCTTC ATGTTCTTAT TTTAGGAGAG GCCAAATTGT TTTTT	1325		
Pro Gly Ser Asn			
370			
GTCATTGGCG TGCACACGTG TGTGTGTGTG TGTGTGTGTG TGTAAGGTGT CTTATAATCT	1385		
TTTACCTATT TCTTACAATT GCAAGATGAC TGGCTTACT ATTTGAAAAC TGGTTTGTGT	1445		
ATCATATCAT ATATCATTAA AGCAGTTGA AGGCATACTT TTGCATAGAA ATAAAAAAA	1505		
TACTGATTG GGGCAATGAG GAATATTGA CAATTAAGTT AATCTTCACG TTTTGCAAA	1565		
CTTTGATTAA TATTCATCT GAACTTGTAA CAAAGATTAA TATTAATAT TTGGCATACA	1625		
AGAGATATGA AAAAAAAA AAAAAAAA A	1656		

(2) INFORMATION FOR SEQ ID NO:15:

54

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 392 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

- (A) NAME/KEY: Signal Sequence

- (B) LOCATION: 1...19

- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Leu Leu Cys
-15 -10 -5
Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp
1 5 10
Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu
15 20 25
Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser
30 35 40 45
Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu
50 55 60
Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg
65 70 75
Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly
80 85 90
Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg
95 100 105
Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe
110 115 120 125
Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys
130 135 140
Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys
145 150 155
Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
160 165 170
Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
175 180 185
Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
190 195 200 205

2455

Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
 210 215 220
 Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
 225 230 235
 Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
 240 245 250
 Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
 255 260 265
 Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
 270 275 280 285
 Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val
 290 295 300
 Tyr Val Arg Met Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile
 305 310 315
 Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
 320 325 330
 Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
 335 340 345
 Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly Asp
 350 355 360 365
 Thr Val Phe Pro Pro Gly Ser Asn
 370

(2) INFORMATION FOR SEQ ID NO:16:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1176 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

ATGGCNGGNA	THCCNGGNYT	NYTNTYYTN	YTNTYYTYY	TNYTNTGYGC	NGTNGGNCAR	60
GTNWSNCNT	AYWSNGCNCC	NTGGAARCCN	ACNTGGCCNG	CNTAYMGNYT	NCCNGTNGTN	120
YTNCCNCARW	SNACNYTNAA	YYTNGCNAAR	CCNGAYTTYG	GNGCNGARGC	NAARYTNGAR	180
GTNWSNWSNW	SNTGYGGNCC	NCARTGYCAY	AARGGNACNC	CNYTNCCNAC	NTAYGARGAR	240
GCNAARCAR	AYYTNWSNTA	YGARACNYTN	TAYGCNAAYG	GNWSNMGNAC	NGARACNCAR	300
GTNGGNATHT	AYATHYTNWS	NWSNWSNGGN	GAYGGNGCNC	ARCAYMGNGA	YWSNGGNWSN	360
WSNNGNARW	SNMGNMGNAA	RMGNCARATH	TAYGGNTAYG	AYWSNMGNTT	YWSNATHTTY	420
GGNAARGAYT	TYYTNYTNAA	YTAYCCNTTY	WSNACNWSNG	TNAARYTNWS	NACNGGNTGY	480
ACNGGNACNY	TNGTNGCNGA	RAARCAYGTN	YTNACNGCNG	CNCAYTGYAT	HCAYGAYGGN	540
AARACNTAYG	TNAARGGNAC	NCARAARYTN	MGNGTNGGNT	TYYTNAARCC	NAARTTYAAR	600
GAYGGNGGNM	GNNGNGCNAA	YGAYWSNACN	WSNGCNATGC	CNGARCARAT	GAARTTYCAR	660

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18 56

TGGATHMGNG	TNAARMGNAC	NCAYGTNCCN	AARGGNTGGA	THAARGGNAA	YGCNAAYGAY	720
ATHGGNATGG	AYTAYGAYTA	YGCNYTNYTN	GARYTNAARA	ARCCNCAYAA	RMGNAARTTY	780
ATGAARATHG	GNGTNWSNCC	NCCNGCNAAR	CARYTNCCNG	GNGGNMGNAT	HCAYTTYWSN	840
GGNTAYGAYA	AYGAYMGNCC	NGGNAAYYTN	GTNTAYMGN	TYTGYGAYGT	NAARGAYGAR	900
ACNTAYGAYY	TNYTNAYCA	RCARTGYGAY	GCNCARCCNG	GNGCNWSNGG	NWSNGGNGTN	960
TAYGTNMGNA	TGTGGAARMG	NCARCARCAR	AARTGGGARM	GNAARATHAT	HGGNATHTTY	1020
WSNGGNACYC	ARTGGGTNGA	YATGAAYGGN	WSNCCNCARG	AYTTYAAYGT	NGCNGTNMGN	1080
ATHACNCCNY	TNAARTAYGC	NCARATHHTGY	TAYTGGATHA	ARGGNAAYTA	YYTNGAYTGY	1140
MGNGARGGNG	AYACNGTNTT	YCCNCCNGGN	WSNAAY			1176

(2) INFORMATION FOR SEQ ID NO:17:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1679 base pairs
- (B) TYPE: nucleic acid
- (C) STRANDEDNESS: double
- (D) TOPOLOGY: linear

(ix) FEATURE:

- (A) NAME/KEY: Coding Sequence
- (B) LOCATION: 111...1259
- (D) OTHER INFORMATION:

- (A) NAME/KEY: Signal Sequence
- (B) LOCATION: 111...167
- (D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GAATTGGCA	CGAGGGGGAG	CCGCGCGCTC	TCTCCCGGCG	CCCACACCTG	TCTGAGCGGC	60
GCAGCGAGCC	GCGGCCCGGG	CGGGCTGCTC	GGCGCGGAAC	AGTGCTCGC	ATG GCA	116
					Met Ala	

GGG ATT CCA GGG CTC CTC TTC CTT CTC TTC TTT CTG CTC TGT GCT GTT	164		
Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys Ala Val			
-15	-10	-5	

GGG CAA GTG AGC CCT TAC AGT GCC CCC TGG AAA CCC ACT TGG CCT GCA	212		
Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp Pro Ala			
1	5	10	15

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2657

TAC CGC CTC CCT GTC GTC TTG CCC CAG TCT ACC CTC AAT TTA GCC AAG		260
Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu Ala Lys		
20	25	30
CCA GAC TTT GGA GCC GAA GCC AAA TTA GAA GTA TCT TCT TCA TGT GGA		308
Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser Cys Gly		
35	40	45
CCC CAG TGT CAT AAG GGA ACT CCA CTG CCC ACT TAC GAA GAG GCC AAG		356
Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu Ala Lys		
50	55	60
CAA TAT CTG TCT TAT GAA ACG CTC TAT GCC AAT GGC AGC CGC ACA GAG		404
Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg Thr Glu		
65	70	75
ACG CAG GTG GGC ATC TAC ATC CTC AGC AGT AGT GGA GAT GGG GCC CAA		452
Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Gly Asp Gly Ala Gln		
80	85	95
CAC CGA GAC TCA GGG TCT TCA GGA AAG TCT CGA AGG AAG CGG CAG ATT		500
His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg Gln Ile		
100	105	110
TAT GGC TAT GAC AGC AGG TTC AGC ATT TTT GGG AAG GAC TTC CTG CTC		548
Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe Leu Leu		
115	120	125
AAC TAC CCT TTC TCA ACA TCA GTG AAG TTA TCC ACG GGC TGC ACC GGC		596
Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys Thr Gly		
130	135	140
ACC CTG GTG GCA GAG AAG CAT GTC CTC ACA GCT GCC CAC TGC ATA CAC		644
Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys Ile His		
145	150	155
GAT GGA AAA ACC TAT GTG AAA GGA ACC CAG AAG CTT CGA GTG GGC TTC		692
Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val Gly Phe		
160	165	170
175		
CTA AAG CCC AAG TTT AAA GAT GGT GGT CGA GGG GCC AAC GAC TCC ACT		740
Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp Ser Thr		
180	185	190

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1758

TCA GCC ATG CCC GAG CAG ATG AAA TTT CAG TGG ATC CGG GTG AAA CGC 788
Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val Lys Arg
195 200 205

ACC CAT GTG CCC AAG GGT TGG ATC AAG GGC AAT GCC AAT GAC ATC GGC 836
Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp Ile Gly
210 215 220

ATG GAT TAT GAT TAT GCC CTC CTG GAA CTC AAA AAG CCC CAC AAG AGA 884
Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His Lys Arg
225 230 235

AAA TTT ATG AAG ATT GGG GTG AGC CCT CCT GCT AAG CAG CTG CCA GGG 932
Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu Pro Gly
240 245 250 255

GGC AGA ATT CAC TTC TCT GGT TAT GAC AAT GAC CGA CCA GGC AAT TTG 980
Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly Asn Leu
260 265 270

GTG TAT CGC TTC TGT GAC GTC AAA GAC GAG ACC TAT GAC TTG CTC TAC 1028
Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu Leu Tyr
275 280 285

CAG CAA TGC GAT GCC CAG CCA GGG GCC AGC GGG TCT GGG GTC TAT GTG 1076
Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val Tyr Val
290 295 300

AGG ATG TGG AAG AGA CAG CAG AAG TGG GAG CGA AAA ATT ATT GGC 1124
Arg Met Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile Ile Gly
305 310 315

ATT TTT TCA GGG CAC CAG TGG GTG GAC ATG AAT GGT TCC CCA CAG GAT 1172
Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro Gln Asp
320 325 330 335

TTC AAC GTG GCT GTC AGA ATC ACT CCT CTC AAA TAT GCC CAG ATC TGC 1220
Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln Ile Cys
340 345 350

TAT TGG ATT AAA GGA AAC TAC CTG GAT TGT AGG GAG GGG TGACACAGTG TT 1271
Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
355 360

CCCTCCTGGC AGCAATTAAG GGTCTTCATG TTCTTATTTT AGGAGAGGCC AAATTGTTTT 1331

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1859

TTGTCATTGG CGTGCACACG	TGTGTGTGTG	TGTGTGTGTG	TGTGTAAGGT	GTCTTATAAT	1391
CTTTTACCTA TTTCTTACAA	TTGCAAGATG	ACTGGCTTTA	CTATTTGAAA	ACTGGTTTGT	1451
GTATCATATC ATATATCATT	TAAGCAGTTT	GAAGGCATAC	TTTGCATAG	AAATAAAAAA	1511
AATACTGATT TGGGGCAATG	AGGAATATTT	GACAATTAAG	TTAATCTTCA	CGTTTTGCA	1571
AACTTGATT TTTATTTCAT	CTGAACTTGT	TTCAAAGATT	TATATTAAT	ATTTGGCATA	1631
CAAGAGATAT GAAAAAAA	AAAAAAA	AAAAATTCCCT	GC GGCCGC		1679

(2) INFORMATION FOR SEQ ID NO:18:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 383 amino acids
- (B) TYPE: amino acid
- (C) STRANDEDNESS: single
- (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(v) FRAGMENT TYPE: internal

(ix) FEATURE:

(A) NAME/KEY: Signal Sequence

(B) LOCATION: 1...19

(D) OTHER INFORMATION:

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

Met Ala Gly Ile Pro Gly Leu Leu Phe Leu Leu Phe Phe Leu Leu Cys			
	-15	-10	-5
Ala Val Gly Gln Val Ser Pro Tyr Ser Ala Pro Trp Lys Pro Thr Trp			
	1	5	10
Pro Ala Tyr Arg Leu Pro Val Val Leu Pro Gln Ser Thr Leu Asn Leu			
	15	20	25
Ala Lys Pro Asp Phe Gly Ala Glu Ala Lys Leu Glu Val Ser Ser Ser			
	30	35	40
Cys Gly Pro Gln Cys His Lys Gly Thr Pro Leu Pro Thr Tyr Glu Glu			
	50	55	60
Ala Lys Gln Tyr Leu Ser Tyr Glu Thr Leu Tyr Ala Asn Gly Ser Arg			
	65	70	75
Thr Glu Thr Gln Val Gly Ile Tyr Ile Leu Ser Ser Ser Gly Asp Gly			
	80	85	90
Ala Gln His Arg Asp Ser Gly Ser Ser Gly Lys Ser Arg Arg Lys Arg			
	95	100	105
Gln Ile Tyr Gly Tyr Asp Ser Arg Phe Ser Ile Phe Gly Lys Asp Phe			
	110	115	120
Leu Leu Asn Tyr Pro Phe Ser Thr Ser Val Lys Leu Ser Thr Gly Cys			
	130	135	140

100

1860

Thr Gly Thr Leu Val Ala Glu Lys His Val Leu Thr Ala Ala His Cys
145 150 155
Ile His Asp Gly Lys Thr Tyr Val Lys Gly Thr Gln Lys Leu Arg Val
160 165 170
Gly Phe Leu Lys Pro Lys Phe Lys Asp Gly Gly Arg Gly Ala Asn Asp
175 180 185
Ser Thr Ser Ala Met Pro Glu Gln Met Lys Phe Gln Trp Ile Arg Val
190 195 200 205
Lys Arg Thr His Val Pro Lys Gly Trp Ile Lys Gly Asn Ala Asn Asp
210 215 220
Ile Gly Met Asp Tyr Asp Tyr Ala Leu Leu Glu Leu Lys Lys Pro His
225 230 235
Lys Arg Lys Phe Met Lys Ile Gly Val Ser Pro Pro Ala Lys Gln Leu
240 245 250
Pro Gly Gly Arg Ile His Phe Ser Gly Tyr Asp Asn Asp Arg Pro Gly
255 260 265
Asn Leu Val Tyr Arg Phe Cys Asp Val Lys Asp Glu Thr Tyr Asp Leu
270 275 280 285
Leu Tyr Gln Gln Cys Asp Ala Gln Pro Gly Ala Ser Gly Ser Gly Val
290 295 300
Tyr Val Arg Met Trp Lys Arg Gln Gln Lys Trp Glu Arg Lys Ile
305 310 315
Ile Gly Ile Phe Ser Gly His Gln Trp Val Asp Met Asn Gly Ser Pro
320 325 330
Gln Asp Phe Asn Val Ala Val Arg Ile Thr Pro Leu Lys Tyr Ala Gln
335 340 345
Ile Cys Tyr Trp Ile Lys Gly Asn Tyr Leu Asp Cys Arg Glu Gly
350 355 360

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